

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 23:02:39 ; Search time 356.058 Seconds
(without alignments)
384.253 Million cell updates/sec

Title: US-10-089-177-697

Perfect score: 23

Sequence: 1 cnaangfckncrcrcyrcrcg 23

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues
Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum March 0%
Maximum March 100%
Listing first 500 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	17.4	75.7	23	US-09-989-643-108
2	17.4	75.7	23	US-10-753-169-108
3	17.4	75.7	24	US-10-391-249-35
4	17.4	75.7	98	US-09-815-242-607
5	17.4	75.7	98	US-10-282-122A-626
6	17.4	75.7	108	US-10-282-122A-2940
7	17.4	75.7	108	US-10-282-122A-3089
8	17.4	75.7	108	US-10-282-122A-3372
9	17.4	75.7	122	US-10-282-122A-1095
c 10	17.4	75.7	186	US-10-282-122A-11867
11	17.4	75.7	298	US-09-815-242-608

12	17.4	75.7	298	US-10-282-122A-633	Sequence 633, App
13	17.4	75.7	305	US-09-815-242-2764	Sequence 2764, App
14	17.4	75.7	305	US-10-282-122A-2664	Sequence 2664, App
15	17.4	75.7	305	US-10-282-122A-5304	Sequence 5304, App
16	17.4	75.7	341	US-10-282-122A-2431	Sequence 2431, App
17	17.4	75.7	383	US-10-282-122A-2253	Sequence 2253, App
c 18	17.4	75.7	402	US-10-282-122A-8376	Sequence 8376, App
c 19	17.4	75.7	402	US-10-282-122A-19466	Sequence 19466, App
c 20	17.4	75.7	447	US-10-282-122A-2476	Sequence 2476, App
c 21	17.4	75.7	448	US-10-282-122A-12826	Sequence 12826, App
c 22	17.4	75.7	468	US-10-282-122A-37380	Sequence 37380, App
c 23	17.4	75.7	882	US-09-989-643-149	Sequence 149, App
c 24	17.4	75.7	882	US-10-391-249-21	Sequence 21, App1
c 25	17.4	75.7	882	US-10-753-169-149	Sequence 149, App
c 26	17.4	75.7	885	US-09-989-643-148	Sequence 148, App
c 27	17.4	75.7	885	US-10-753-169-148	Sequence 148, App
c 28	17.4	75.7	887	US-10-391-249-20	Sequence 20, App1
c 29	17.4	75.7	888	US-09-989-643-152	Sequence 152, App
c 30	17.4	75.7	888	US-10-753-169-152	Sequence 152, App
c 31	17.4	75.7	891	US-09-989-643-154	Sequence 154, App
c 32	17.4	75.7	891	US-09-989-643-155	Sequence 155, App
c 33	17.4	75.7	891	US-10-753-169-159	Sequence 159, App
c 34	17.4	75.7	891	US-09-989-643-157	Sequence 157, App
c 35	17.4	75.7	891	US-09-989-643-159	Sequence 159, App
c 36	17.4	75.7	891	US-09-989-643-160	Sequence 160, App
c 37	17.4	75.7	891	US-09-989-643-161	Sequence 161, App
c 38	17.4	75.7	891	US-09-989-643-162	Sequence 162, App
c 39	17.4	75.7	891	US-09-989-643-163	Sequence 163, App
c 40	17.4	75.7	891	US-09-989-643-164	Sequence 164, App
c 41	17.4	75.7	891	US-10-753-169-154	Sequence 154, App
c 42	17.4	75.7	891	US-10-753-169-155	Sequence 155, App
c 43	17.4	75.7	891	US-10-753-169-157	Sequence 157, App
c 44	17.4	75.7	891	US-10-753-169-159	Sequence 159, App
c 45	17.4	75.7	891	US-10-753-169-160	Sequence 160, App
c 46	17.4	75.7	891	US-10-753-169-161	Sequence 161, App
c 47	17.4	75.7	891	US-10-753-169-162	Sequence 162, App
c 48	17.4	75.7	891	US-10-753-169-163	Sequence 163, App
c 49	17.4	75.7	894	US-10-753-169-164	Sequence 164, App
c 50	17.4	75.7	894	US-09-989-643-151	Sequence 151, App
c 51	17.4	75.7	894	US-09-989-643-156	Sequence 156, App
c 52	17.4	75.7	894	US-09-989-643-167	Sequence 167, App
c 53	17.4	75.7	894	US-10-753-169-151	Sequence 151, App
c 54	17.4	75.7	894	US-10-753-169-156	Sequence 156, App
c 55	17.4	75.7	897	US-10-753-169-167	Sequence 167, App
c 56	17.4	75.7	897	US-09-989-643-147	Sequence 147, App
c 57	17.4	75.7	897	US-09-989-643-166	Sequence 166, App
c 58	17.4	75.7	897	US-09-989-643-168	Sequence 168, App
c 59	17.4	75.7	897	US-10-753-169-147	Sequence 147, App
c 60	17.4	75.7	897	US-10-753-169-166	Sequence 166, App
c 61	17.4	75.7	906	US-09-989-643-158	Sequence 158, App
c 62	17.4	75.7	906	US-09-989-643-158	Sequence 158, App
c 63	17.4	75.7	909	US-10-753-169-158	Sequence 158, App
c 64	17.4	75.7	909	US-09-989-643-171	Sequence 171, App
c 65	17.4	75.7	918	US-10-753-169-171	Sequence 171, App
c 66	17.4	75.7	950	US-10-282-122A-23136	Sequence 23136, App
c 67	17.4	75.7	950	US-10-282-122A-23136	Sequence 23136, App
c 68	17.4	75.7	1170	US-10-156-761-7006	Sequence 7006, App
c 69	17.4	75.7	1182	US-09-815-242-4519	Sequence 4519, App
c 70	17.4	75.7	1182	US-10-282-122A-12755	Sequence 12755, App
c 71	17.4	75.7	1182	US-10-282-122A-19744	Sequence 19744, App
c 72	17.4	75.7	1182	US-10-282-122A-23175	Sequence 23175, App
c 73	17.4	75.7	1182	US-10-282-122A-29330	Sequence 29330, App
c 74	17.4	75.7	1182	US-10-282-122A-32228	Sequence 32228, App
c 75	17.4	75.7	1182	US-10-282-122A-33485	Sequence 33485, App
c 76	17.4	75.7	1182	US-10-282-122A-35489	Sequence 35489, App
c 77	17.4	75.7	1182	US-10-470-0488-115	Sequence 115, App
c 78	17.4	75.7	1185	US-10-282-122A-37061	Sequence 37061, App
c 79	17.4	75.7	1185	US-09-912-020-86	Sequence 86, App1
c 80	17.4	75.7	1185	US-09-815-242-3832	Sequence 3832, App
c 81	17.4	75.7	1185	US-09-815-242-6265	Sequence 6265, App
c 82	17.4	75.7	1185	US-09-815-242-6334	Sequence 6334, App
c 83	17.4	75.7	1185	US-09-815-242-6962	Sequence 6962, App
c 84	17.4	75.7	1185	US-09-815-242-6972	Sequence 6972, App
c 85	17.4	75.7	1185	US-09-815-242-8344	Sequence 8344, App

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OM nucleic - nucleic search, using sw model

Run on: March 16, 2005, 01:07:34 ; Search time 87.1346 Seconds
(without alignments)
431.911 Million cell updates/sec

Title: US-10-089-177-697

Perfect score: 23

Sequence: 1 ccmagntnckncrcrcrcrcg 23

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 81818359 residues

Total number of hits satisfying chosen parameterb: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17.4	75.7	189	US-09-107-532A-3602	Sequence 3602, Ap
2	17.4	75.7	297	US-09-252-991A-4695	Sequence 4695, Ap
3	17.4	75.7	330	US-09-107-532A-1603	Sequence 1603, Ap
4	17.4	75.7	498	US-09-902-540-7475	Sequence 7475, Ap
5	17.4	75.7	609	US-09-107-433-2243	Sequence 2243, Ap
6	17.4	75.7	785	US-09-154-083-229	Sequence 29, Appl
7	17.4	75.7	1122	US-09-134-000C-1261	Sequence 1261, Ap
8	17.4	75.7	1131	US-09-107-532A-979	Sequence 979, Appl
9	17.4	75.7	1135	US-09-328-352-1547	Sequence 1547, Ap
10	17.4	75.7	1185	US-08-743-637B-185	Sequence 185, Appl
11	17.4	75.7	1185	US-09-218-197-1	Sequence 1, Appl
12	17.4	75.7	1185	US-09-492-709A-86	Sequence 86, Appl
13	17.4	75.7	1191	US-09-107-532A-1379	Sequence 1379, Appl
14	17.4	75.7	1191	US-09-902-540-8380	Sequence 8380, Ap
15	17.4	75.7	1197	US-09-583-110-747	Sequence 747, Appl
16	17.4	75.7	1224	US-09-452-991A-4775	Sequence 4775, Ap
17	17.4	75.7	1230	US-09-252-991A-4733	Sequence 4733, Ap
18	17.4	75.7	1230	US-09-252-991A-4767	Sequence 4767, Ap
19	17.4	75.7	1245	US-09-134-001C-2540	Sequence 2540, Ap
20	17.4	75.7	1254	US-09-489-039A-3750	Sequence 3750, Ap
21	17.4	75.7	1260	US-09-489-039A-3750	Sequence 3750, Ap
22	17.4	75.7	1356	US-09-252-991A-4740	Sequence 4740, Ap
23	17.4	75.7	2996	US-08-961-527-260	Sequence 260, Appl
24	17.4	75.7	3719	US-08-920-812-10	Sequence 10, Appl
25	17.4	75.7	3719	US-08-920-827-10	Sequence 10, Appl
26	17.4	75.7	3719	US-08-921-177-10	Sequence 10, Appl
27	17.4	75.7	3719	US-08-362-577C-10	Sequence 10, Appl

28	17.4	75.7	3719	US-08-920-828-10	Sequence 10, Appl
29	17.4	75.7	5787	US-09-902-540-722	Sequence 722, Appl
30	17.4	75.7	7035	US-09-902-540-878	Sequence 878, Appl
31	17.4	75.7	15598	US-08-956-171E-82	Sequence 82, Appl
32	17.4	75.7	15598	US-08-781-986A-82	Sequence 82, Appl
33	17.4	75.7	49617	US-09-596-002-28	Sequence 28, Appl
34	17.4	75.7	580073	US-08-545-528D-1	Sequence 1, Appl
35	17.4	75.7	640681	US-08-790-988-1	Sequence 1, Appl
36	17.4	75.7	1830121	US-09-557-884-1	Sequence 1, Appl
37	17.4	75.7	1830121	US-09-557-884-1	Sequence 1, Appl
38	17.4	75.7	1830121	US-09-643-990A-1	Sequence 1, Appl
39	17.4	75.7	1830121	US-09-643-990A-1	Sequence 1, Appl
40	17.4	75.7	4403765	US-09-103-840A-2	Sequence 2, Appl
41	17.4	75.7	4411529	US-09-103-840A-1	Sequence 1, Appl
42	15.8	68.7	489	US-09-252-991A-10298	Sequence 10298, A
43	15.8	68.7	601	US-09-949-016-204917	Sequence 204917, A
44	15.8	68.7	601	US-09-949-016-204917	Sequence 204917, A
45	15.8	68.7	651	US-09-902-540-4369	Sequence 4369, Ap
46	15.8	68.7	1689	US-09-902-540-3347	Sequence 3347, Ap
47	15.8	68.7	3231	US-08-074-121-4	Sequence 4, Appl
48	15.8	68.7	3231	PCT-US94-06447-4	Sequence 4, Appl
49	15.8	68.7	9790	US-09-643-238-401	Sequence 401, A
50	15.8	68.7	11935	US-09-949-016-17204	Sequence 17204, A
51	15.8	68.7	12001	US-08-458-568A-11	Sequence 11, Appl
52	15.8	68.7	12887	US-09-949-016-17203	Sequence 17203, A
53	15.8	68.7	18537	US-09-902-540-1157	Sequence 1157, Ap
54	15.8	68.7	23694	US-09-902-540-1216	Sequence 1216, Ap
55	15.8	68.7	31063	US-09-596-002-20	Sequence 20, Appl
56	15.8	68.7	39376	US-09-949-016-17536	Sequence 17536, A
57	15.8	68.7	1230025	US-09-198-452A-1	Sequence 1, Appl
58	15.8	68.7	1230230	US-09-438-185A-1	Sequence 1, Appl
59	15.8	68.7	4403765	US-09-103-840A-1	Sequence 2, Appl
60	15.8	68.7	4411529	US-09-103-840A-1	Sequence 1, Appl
61	15.2	66.3	5198	US-08-123-761A-1	Sequence 1, Appl
62	14.8	64.3	30	US-08-207-901-13	Sequence 13, Appl
63	14.8	64.3	341	US-09-621-976-2404	Sequence 2404, Ap
64	14.8	64.3	601	US-09-949-016-169225	Sequence 169225, A
65	14.8	64.3	601	US-09-949-016-186119	Sequence 186119, A
66	14.8	64.3	867	US-09-902-540-6042	Sequence 6042, Ap
67	14.8	64.3	870	US-09-902-540-243	Sequence 243, Appl
68	14.8	64.3	933	US-09-902-540-9341	Sequence 9341, Ap
69	14.8	64.3	1044	US-09-902-540-9341	Sequence 9341, Ap
70	14.8	64.3	1430	US-09-976-354-878	Sequence 878, Appl
71	14.8	64.3	1509	US-09-602-777A-211	Sequence 211, Appl
72	14.8	64.3	2007	US-09-902-540-8607	Sequence 8607, Ap
73	14.8	64.3	2286	US-09-800-729-43	Sequence 43, Appl
74	14.8	64.3	2329	US-09-800-729-11	Sequence 11, Appl
75	14.8	64.3	2355	US-09-902-540-909	Sequence 909, Appl
76	14.8	64.3	6961	US-09-949-016-4770	Sequence 4770, Ap
77	14.8	64.3	7552	US-09-902-540-997	Sequence 997, Appl
78	14.8	64.3	1486	US-09-949-016-17047	Sequence 17047, A
79	14.8	64.3	14516	US-09-949-016-14927	Sequence 14927, A
80	14.8	64.3	45314	US-09-949-016-16512	Sequence 16512, A
81	14.8	64.3	52218	US-09-335-409-1	Sequence 1, Appl
82	14.8	64.3	66750	US-09-568-102-1	Sequence 1, Appl
83	14.8	64.3	66750	US-09-567-969-1	Sequence 1, Appl
84	14.8	64.3	66750	US-09-567-969-1	Sequence 1, Appl
85	14.8	64.3	66750	US-09-568-480-1	Sequence 1, Appl
86	14.8	64.3	66750	US-09-568-480-1	Sequence 1, Appl
87	14.8	64.3	66750	US-09-568-472-1	Sequence 1, Appl
88	14.8	64.3	66750	US-09-568-472-1	Sequence 1, Appl
89	14.8	64.3	66750	US-09-568-472-1	Sequence 1, Appl
90	14.8	64.3	100836	US-09-949-016-12871	Sequence 12871, A
91	14.8	64.3	100837	US-09-949-016-17063	Sequence 17063, A
92	14.6	63.5	574	US-09-073-297-23	Sequence 23, Appl
93	14.6	63.5	574	US-09-949-016-18180	Sequence 918180, A
94	14.6	63.5	601	US-09-949-016-194751	Sequence 194751, A
95	14.6	63.5	1299	US-09-902-540-1780	Sequence 4780, Ap
96	14.6	63.5	1188	US-09-902-540-1166	Sequence 1166, Ap
97	14.6	63.5	27903	US-09-902-540-1235	Sequence 1235, Ap
98	14.6	63.5	197336	US-09-949-016-12881	Sequence 12881, A
99	14.6	63.5	197337	US-09-949-016-14376	Sequence 14376, A
100	14.6	63.5	234288	US-09-949-016-17272	Sequence 17272, A

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 22:27:13 ; Search time 2312.38 seconds
(without alignments)
378.604 Million cell updates/sec

Title: US-10-089-177-697

Perfect score: 23

Sequence: 1 cnaacnctknccrcycrcg 23

Scoring table: IDENTITY_NUC

Gapped 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
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8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17.4	75.7	190	6	CD163898 ML1-0084T
C 2	17.4	75.7	259	6	CD180022 MS1-0021T
C 3	17.4	75.7	365	7	CN028509 UMC-Pb11v
C 4	17.4	75.7	372	7	CN026743 UMC-Pd11v
C 5	17.4	75.7	422	1	AU007630 AU007630
C 6	17.4	75.7	465	1	AU010926 AU010926
C 7	17.4	75.7	518	5	BQ811177 103002180
C 8	17.4	75.7	527	5	BQ821806 103009550
C 9	17.4	75.7	539	5	BQ812860 103005320
C 10	17.4	75.7	566	5	BQ815804 103005310
C 11	17.4	75.7	570	8	CC107141 ND1.13F13
C 12	17.4	75.7	579	5	BQ809961 103001400
C 13	17.4	75.7	626	5	BQ809962 103001400
C 14	17.4	75.7	637	5	BQ811176 103002180
C 15	17.4	75.7	712	7	CO755154 M41R3048
C 16	17.4	75.7	718	7	CO255523 W500825.B
C 17	17.4	75.7	777	9	CL695862 PR1017C.B
C 18	17.4	75.7	1122	8	BZ549591 Pac81-60
C 19	16.4	71.3	424	6	CB302180 TGEStzyf9
C 20	16.4	71.3	471	6	CB302236 TGEStzyf9
C 21	16.4	71.3	505	2	BF252980 EST445475
C 22	16.4	71.3	531	7	CO151838 EST826891
C 23	16.4	71.3	538	6	CA153033 SCJPR2203
C 24	16.4	71.3	545	7	CF939964 NESTGabs

C 25	16.4	71.3	556	7	CF883816 tr1c035xo
C 26	16.4	71.3	582	5	BP176275 BP176275
C 27	16.4	71.3	589	7	CO134814 EST829485
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C 29	16.4	71.3	614	7	CO151287 EST826340
C 30	16.4	71.3	637	7	CF387912 RTDR1_17
C 31	16.4	71.3	748	7	CV516454 0048P0015
C 32	16.4	71.3	766	7	CO005587 EST793922
C 33	16.4	71.3	759	7	CF816095 EST693477
C 34	16.4	71.3	784	7	CO005588 EST793923
C 35	16.4	71.3	801	8	BZ54176 OGAOT931M
C 36	16.4	71.3	844	7	CO013017 EST801352
C 37	16.4	71.3	862	7	CO006264 EST794599
C 38	16.4	71.3	864	7	CO035000 EST813384
C 39	16.4	71.3	874	2	BP210517 601874743
C 40	16.4	71.3	885	7	CO005704 EST794039
C 41	16.4	71.3	912	7	CF822001 EST699383
C 42	16.4	71.3	917	7	CO024761 EST803145
C 43	16.4	71.3	943	7	CO005703 EST794038
C 44	16.4	71.3	965	7	CO013018 EST801353
C 45	16.4	71.3	993	7	CO011949 EST800284
C 46	16.4	71.3	997	7	CO012398 EST800733
C 47	16.4	71.3	1021	7	CO013654 EST801989
C 48	16.4	71.3	1035	7	CO009743 EST798078
C 49	16.4	71.3	1052	7	CO009560 EST797895
C 50	16.2	70.4	372	2	BE012230 945015F07
C 51	16.2	70.4	453	5	BK548810 BK548810
C 52	16.2	70.4	521	7	CO373708 NMR019D02
C 53	16.2	70.4	527	1	AU294800 AU294800
C 54	16.2	70.4	527	5	BUS682391 946188H06
C 55	16.2	70.4	537	6	CB603919 3529.1.53
C 56	16.2	70.4	545	2	AM065506 614056B07
C 57	16.2	70.4	581	7	CO51316 3530.1.20
C 58	16.2	70.4	593	6	CA293879 SCSEGV100
C 59	16.2	70.4	598	5	BQ295679 109104181
C 60	16.2	70.4	601	6	CA157547 SCEZR2301
C 61	16.2	70.4	602	6	CA144349 SCRRRT201
C 62	16.2	70.4	605	6	CA828642 1114031C0
C 63	16.2	70.4	606	1	AU295857 AU295857
C 64	16.2	70.4	609	2	AM037181 614021B08
C 65	16.2	70.4	620	6	CD428143 ETH1_32.F
C 66	16.2	70.4	620	6	CA190991 SCCRT2C0
C 67	16.2	70.4	632	5	CA078183 SCRFAM102
C 68	16.2	70.4	632	5	BQ487172 1091051P1
C 69	16.2	70.4	659	6	CA213034 SCBSST310
C 70	16.2	70.4	668	7	CA153871 SCVPR2203
C 71	16.2	70.4	668	7	CK863732 35011.In
C 72	16.2	70.4	671	7	CV472864 21014.1.D
C 73	16.2	70.4	676	6	CB669932 OSJNE02M
C 74	16.2	70.4	704	7	CK765620 aam01-5ms
C 75	16.2	70.4	710	4	BG464592 EMI_71.F1
C 76	16.2	70.4	722	5	BQ087411 Cr1_10.D0
C 77	16.2	70.4	730	7	CN203557 T03852.G
C 78	16.2	70.4	737	7	CN149202 WOUNDI_61
C 79	16.2	70.4	738	7	CN149631 WOUNDI_64
C 80	16.2	70.4	741	6	CB635325 OS1EB15T
C 81	16.2	70.4	796	4	BG319815 Zm03_0810
C 82	16.2	70.4	813	6	CB634299 OS1EB13L
C 83	16.2	70.4	814	4	CN145755 WOUNDI_35
C 84	16.2	70.4	827	6	CA276170 SCCCSDI09
C 85	16.2	70.4	835	9	CG183637 PUFZK36TD
C 86	16.2	70.4	936	9	CG101716 FUFKX95TB
C 87	16.2	70.4	1192	5	BQ212311 AGENCOURT
C 88	16.2	70.4	1255	3	AY108591 Zea_mays
C 89	16.2	70.4	1666	2	BG025600 602274526
C 90	15.8	68.7	138	2	BE518692 946074C08
C 91	15.8	68.7	222	4	BJS46812 BJS46812
C 92	15.8	68.7	224	4	BJS46790 BJS46790
C 93	15.8	68.7	249	1	AV943089 AV943089
C 94	15.8	68.7	259	1	AV084980 AV084980
C 95	15.8	68.7	264	6	CA681688 wlm24.DK0
C 96	15.8	68.7	268	1	AU248181 AU248181
C 97	15.8	68.7	272	6	CA282200 SCAGSD204

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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 15:46:58 ; Search time 296.346 Seconds
(without alignments)
459.443 Million cell updates/sec

Title: US-10-089-177-697

Perfect score: 23

Sequence: 1 ccaacgfnckncrcrcycrcg 23

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : N_Geneseq_16Dec04:*

- 1: geneseqn19808:*
- 2: geneseqn19908:*
- 3: geneseqn20008:*
- 4: geneseqn20018:*
- 5: geneseqn20028:*
- 6: geneseqn20038:*
- 7: geneseqn20048:*
- 8: geneseqn20058:*
- 9: geneseqn20068:*
- 10: geneseqn20078:*
- 11: geneseqn20088:*
- 12: geneseqn20098:*
- 13: geneseqn20108:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.4	75.7	23	2	AAV37107 Oligonuc
2	17.4	75.7	23	2	AAH0706 Universal
3	17.4	75.7	24	10	ACPS8471 M. hyo
4	17.4	75.7	98	4	AA848030 Enteroc
5	17.4	75.7	98	8	ACA12756 Prokary
6	17.4	75.7	108	8	ACA15502 Prokary
7	17.4	75.7	108	8	ACA15219 Prokary
8	17.4	75.7	108	8	ACA15070 Prokary
9	17.4	75.7	122	8	ACA13225 Prokary
10	17.4	75.7	135	6	ABN69463 Strepto
11	17.4	75.7	186	8	ACA23997 Prokary
12	17.4	75.7	189	10	ADC93975 E. faec
13	17.4	75.7	297	11	ABD06091 Pseudom
14	17.4	75.7	298	8	AA848031 Enteroc
15	17.4	75.7	298	8	ACA12763 Prokary
16	17.4	75.7	305	4	AA850187 Staphylo
17	17.4	75.7	305	8	ACA14824 Prokary
18	17.4	75.7	305	8	ACA17434 Prokary
19	17.4	75.7	330	10	ADC91976 E. faec
20	17.4	75.7	341	8	ACA14561 Prokary

21	17.4	75.7	383	8	ACA14383 Prokary
22	17.4	75.7	402	8	ACA20506 Prokary
23	17.4	75.7	402	8	ACA31596 Prokary
24	17.4	75.7	402	10	AB241635 N. gonorr
25	17.4	75.7	402	10	AB241635 N. gonorr
26	17.4	75.7	447	8	ACA14606 Prokary
27	17.4	75.7	448	8	ACA24956 Prokary
28	17.4	75.7	468	8	ACA49510 Prokary
29	17.4	75.7	476	5	AA889338 DNA encod
30	17.4	75.7	567	10	AB241132 N. gonorr
31	17.4	75.7	567	10	AB241633 N. gonorr
32	17.4	75.7	609	13	ADR93608 Novel S.
33	17.4	75.7	693	3	ABX66003 Helicobac
34	17.4	75.7	785	4	AA889144 Polyketid
35	17.4	75.7	882	2	AAV37148 DNA seque
36	17.4	75.7	882	4	AAH01743 Bacteroid
37	17.4	75.7	885	2	AAV37147 DNA seque
38	17.4	75.7	885	2	AAH01742 Bacillus
39	17.4	75.7	888	2	AAV37151 DNA seque
40	17.4	75.7	888	4	AAH01746 Chlamydia
41	17.4	75.7	888	4	AAH01762 Burkholder
42	17.4	75.7	891	2	AAV37160 DNA seque
43	17.4	75.7	891	2	AAV37156 DNA seque
44	17.4	75.7	891	2	AAV37163 DNA seque
45	17.4	75.7	891	2	AAV37153 DNA seque
46	17.4	75.7	891	2	AAV37161 DNA seque
47	17.4	75.7	891	2	AAV37154 DNA seque
48	17.4	75.7	891	2	AAV37158 DNA seque
49	17.4	75.7	891	2	AAV37159 DNA seque
50	17.4	75.7	891	2	AAV37162 DNA seque
51	17.4	75.7	891	4	AAH01750 Micrococc
52	17.4	75.7	891	4	AAH01754 Rickettsi
53	17.4	75.7	891	4	AAH01752 Mycoplasma
54	17.4	75.7	891	4	AAH01675 Escherich
55	17.4	75.7	891	4	AAH01753 Neisseria
56	17.4	75.7	891	4	AAH01751 Mycobacte
57	17.4	75.7	891	4	AAH00619 Haemophil
58	17.4	75.7	891	4	AAH01755 Salmonell
59	17.4	75.7	891	4	AAH01747 Fibrobact
60	17.4	75.7	894	2	AAV37155 DNA seque
61	17.4	75.7	894	2	AAV37150 DNA seque
62	17.4	75.7	894	2	AAV37166 DNA seque
63	17.4	75.7	894	4	AAH01745 Brevibact
64	17.4	75.7	894	4	AAH01011 Streptoco
65	17.4	75.7	894	4	AAH01748 Flavobact
66	17.4	75.7	894	5	AA889341 DNA encod
67	17.4	75.7	894	5	AA889387 DNA encod
68	17.4	75.7	895	5	AA881954 DNA encod
69	17.4	75.7	895	5	AA881927 DNA encod
70	17.4	75.7	897	2	AAV37165 DNA seque
71	17.4	75.7	897	2	AAV37167 DNA seque
72	17.4	75.7	897	2	AAV37146 DNA seque
73	17.4	75.7	897	4	AAH01757 Stigmater
74	17.4	75.7	897	4	AAH01741 Agrobacte
75	17.4	75.7	897	4	AAH01758 Thiomonas
76	17.4	75.7	900	4	AAH02145 Pseudomon
77	17.4	75.7	906	2	AAV37157 DNA seque
78	17.4	75.7	906	4	AAH01749 Helicobac
79	17.4	75.7	909	2	AAV37170 DNA seque
80	17.4	75.7	909	4	AAH01761 Molinella
81	17.4	75.7	918	8	ACA43747 Prokary
82	17.4	75.7	950	8	ACA35266 Prokary
83	17.4	75.7	968	2	AAV90742 Nucleotid
84	17.4	75.7	970	2	AAV90873 Nucleotid
85	17.4	75.7	1098	10	AB241687 N. gonorr
86	17.4	75.7	1098	10	AB241687 N. gonorr
87	17.4	75.7	1105	6	AB896108 Schizosac
88	17.4	75.7	1122	10	ADH83376 Enterococ
89	17.4	75.7	1131	10	ADH83376 Enterococ
90	17.4	75.7	1155	9	ADA30260 DNA encod
91	17.4	75.7	1170	2	AAO20217 Sequence
92	17.4	75.7	1182	4	AA851937 Staphyloc
93	17.4	75.7	1182	8	ABT14914 Pathogen

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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 22:08:52 ; Search time 874.442 Seconds
(without alignments)
1274.492 Million cell updates/sec

Title: US-10-089-177-697

Perfect score: 23
Sequence: 1 ccaacgcnckncrcrcycrcg 23

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 23
9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Genembl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.4	75.7	23	6	AX109964 Sequence
2	17.4	75.7	23	6	BD023040 Sequence
3	17.4	75.7	135	6	C0649882 Sequence
4	17.4	75.7	189	6	AR348991 Sequence
5	17.4	75.7	330	6	AR346992 Sequence
6	17.4	75.7	485	1	SMU75481 Sequence
7	17.4	75.7	693	6	AX788739 Sequence
8	17.4	75.7	723	1	SPRPS10A Sequence
9	17.4	75.7	762	1	AF295388 Sequence
10	17.4	75.7	882	6	AX111003 Sequence
11	17.4	75.7	882	6	BD023081 Sequence
12	17.4	75.7	885	6	AX111002 Sequence
13	17.4	75.7	885	6	BD023080 Sequence
14	17.4	75.7	888	6	AX111006 Sequence
15	17.4	75.7	888	6	AX111022 Sequence
16	17.4	75.7	888	6	BD023084 Sequence
17	17.4	75.7	891	6	AX109877 Sequence
18	17.4	75.7	891	6	AX110935 Sequence
19	17.4	75.7	891	6	AX111007 Sequence

C 20	17.4	75.7	891	6	AX111010 Sequence
C 21	17.4	75.7	891	6	AX111011 Sequence
C 22	17.4	75.7	891	6	AX111012 Sequence
C 23	17.4	75.7	891	6	AX111013 Sequence
C 24	17.4	75.7	891	6	AX111014 Sequence
C 25	17.4	75.7	891	6	AX111015 Sequence
C 26	17.4	75.7	891	6	BD023086 Sequence
C 27	17.4	75.7	891	6	BD023087 Sequence
C 28	17.4	75.7	891	6	BD023089 Sequence
C 29	17.4	75.7	891	6	BD023091 Sequence
C 30	17.4	75.7	891	6	BD023092 Sequence
C 31	17.4	75.7	891	6	BD023093 Sequence
C 32	17.4	75.7	891	6	BD023094 Sequence
C 33	17.4	75.7	891	6	BD023095 Sequence
C 34	17.4	75.7	891	6	BD023096 Sequence
C 35	17.4	75.7	894	6	AX111026 Sequence
C 36	17.4	75.7	894	6	AX111005 Sequence
C 37	17.4	75.7	894	6	AX111008 Sequence
C 38	17.4	75.7	894	6	BD023083 Sequence
C 39	17.4	75.7	894	6	BD023088 Sequence
C 40	17.4	75.7	894	6	BD023099 Sequence
C 41	17.4	75.7	897	6	AX111017 Sequence
C 42	17.4	75.7	897	6	AX111011 Sequence
C 43	17.4	75.7	897	6	AX111018 Sequence
C 44	17.4	75.7	897	6	BD023079 Sequence
C 45	17.4	75.7	897	6	BD023098 Sequence
C 46	17.4	75.7	897	6	BD023100 Sequence
C 47	17.4	75.7	900	6	AX111405 Sequence
C 48	17.4	75.7	906	6	AX111009 Sequence
C 49	17.4	75.7	906	6	BD023090 Sequence
C 50	17.4	75.7	909	6	AX111021 Sequence
C 51	17.4	75.7	909	6	BD023103 Sequence
C 52	17.4	75.7	968	6	BD061867 Sequence
C 53	17.4	75.7	970	6	BD061998 Sequence
C 54	17.4	75.7	1043	2	PFMAL8PC1 Sequence
C 55	17.4	75.7	1122	1	AR395246 Sequence
C 56	17.4	75.7	1122	1	FGS85RTUF Sequence
C 57	17.4	75.7	1131	6	AR346368 Sequence
C 58	17.4	75.7	1140	1	SASGALTUF Sequence
C 59	17.4	75.7	1143	1	AF295387 Sequence
C 60	17.4	75.7	1149	1	CA636RTUF Sequence
C 61	17.4	75.7	1155	6	AR318997 Sequence
C 62	17.4	75.7	1176	1	AY099292 Sequence
C 63	17.4	75.7	1176	1	AY099294 Sequence
C 64	17.4	75.7	1176	1	AY099295 Sequence
C 65	17.4	75.7	1182	1	AX583738 Sequence
C 66	17.4	75.7	1182	6	AX620422 Sequence
C 67	17.4	75.7	1185	6	AR089426 Sequence
C 68	17.4	75.7	1185	6	BD268414 Sequence
C 69	17.4	75.7	1185	6	C0817257 Sequence
C 70	17.4	75.7	1185	6	C0817259 Sequence
C 71	17.4	75.7	1185	6	AR230091 Sequence
C 72	17.4	75.7	1185	6	AR493528 Sequence
C 73	17.4	75.7	1185	6	AX109965 Sequence
C 74	17.4	75.7	1185	6	AX111364 Sequence
C 75	17.4	75.7	1185	6	AX363591 Sequence
C 76	17.4	75.7	1185	12	AY305395 Sequence
C 77	17.4	75.7	1185	12	AY305396 Sequence
C 78	17.4	75.7	1185	12	AY305397 Sequence
C 79	17.4	75.7	1188	12	AY305399 Sequence
C 80	17.4	75.7	1188	1	AB035461 Sequence
C 81	17.4	75.7	1188	1	AB035462 Sequence
C 82	17.4	75.7	1188	1	AB035463 Sequence
C 83	17.4	75.7	1188	1	AB035464 Sequence
C 84	17.4	75.7	1188	1	AB035465 Sequence
C 85	17.4	75.7	1188	1	AB035466 Sequence
C 86	17.4	75.7	1188	1	TOTUF Sequence
C 87	17.4	75.7	1188	1	CLTUF Sequence
C 88	17.4	75.7	1188	1	FP13524 Sequence
C 89	17.4	75.7	1191	1	AB073986 Sequence
C 90	17.4	75.7	1191	1	TCHEOSTUF Sequence
C 91	17.4	75.7	1191	6	AR346768 Sequence
C 92	17.4	75.7	1191	6	AX110130 Sequence

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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 23:02:39 / Search time 448.942 Seconds
(without alignments)
384.253 Million cell updates/sec

Title: US-10-089-177-664

Perfect score: 29
Sequence: 1 aaygatnagngngngncncaratgga 29

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 311075104

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database:

Published Applications NA.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
5: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10F_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23.2	80.0	29	US-09-989-643-107	Sequence 107, App
2	23.2	80.0	18	US-10-753-169-107	Sequence 107, App
3	23.2	80.0	70	US-10-282-122A-1961	Sequence 1961, App
4	23.2	80.0	70	US-10-282-122A-1961	Sequence 1961, App
5	23.2	80.0	70	US-10-282-122A-2519	Sequence 2519, App
6	23.2	80.0	111	US-10-282-122A-2727	Sequence 2727, App
7	23.2	80.0	130	US-09-815-242-2973	Sequence 2973, App
8	23.2	80.0	130	US-10-282-122A-5535	Sequence 5535, App
9	23.2	80.0	163	US-09-815-242-261	Sequence 261, App
10	23.2	80.0	163	US-10-282-122A-2556	Sequence 2556, App
11	23.2	80.0	183	US-10-282-122A-2416	Sequence 2416, App

C 12	23.2	80.0	184	9	US-09-815-242-2185	Sequence 2185, App
C 13	23.2	80.0	184	17	US-10-282-122A-4758	Sequence 4758, App
C 14	23.2	80.0	185	17	US-10-282-122A-1866	Sequence 1866, App
C 15	23.2	80.0	185	17	US-10-282-122A-2139	Sequence 2139, App
C 16	23.2	80.0	187	9	US-09-815-242-194	Sequence 194, App
C 17	23.2	80.0	187	9	US-09-815-242-198	Sequence 198, App
C 18	23.2	80.0	187	17	US-10-282-122A-184	Sequence 184, App
C 19	23.2	80.0	187	17	US-10-282-122A-202	Sequence 202, App
C 20	23.2	80.0	193	17	US-10-282-122A-2553	Sequence 2553, App
C 21	23.2	80.0	196	17	US-10-282-122A-3396	Sequence 3396, App
C 22	23.2	80.0	202	9	US-09-815-242-176	Sequence 176, App
C 23	23.2	80.0	202	17	US-10-282-122A-164	Sequence 164, App
C 24	23.2	80.0	222	17	US-10-282-122A-1777	Sequence 1777, App
C 25	23.2	80.0	222	17	US-10-282-122A-2570	Sequence 2570, App
C 26	23.2	80.0	236	9	US-09-815-242-301	Sequence 301, App
C 27	23.2	80.0	236	17	US-10-282-122A-280	Sequence 280, App
C 28	23.2	80.0	269	9	US-09-815-242-242	Sequence 242, App
C 29	23.2	80.0	269	17	US-10-282-122A-229	Sequence 229, App
C 30	23.2	80.0	275	17	US-10-282-122A-1789	Sequence 1789, App
C 31	23.2	80.0	275	17	US-10-282-122A-1952	Sequence 1952, App
C 32	23.2	80.0	275	17	US-10-282-122A-2705	Sequence 2705, App
C 33	23.2	80.0	277	9	US-09-294-093B-405	Sequence 405, App
C 34	23.2	80.0	329	17	US-10-282-122A-2708	Sequence 2708, App
C 35	23.2	80.0	332	17	US-10-282-122A-2146	Sequence 2146, App
C 36	23.2	80.0	341	17	US-10-282-122A-2394	Sequence 2394, App
C 37	23.2	80.0	341	17	US-10-282-122A-2527	Sequence 2527, App
C 38	23.2	80.0	343	17	US-10-282-122A-1933	Sequence 1933, App
C 39	23.2	80.0	369	17	US-10-282-122A-2252	Sequence 2252, App
C 40	23.2	80.0	390	17	US-10-282-122A-2619	Sequence 2619, App
C 41	23.2	80.0	501	17	US-10-424-599-79597	Sequence 79597, App
C 42	23.2	80.0	566	17	US-10-282-122A-19211	Sequence 19211, App
C 43	23.2	80.0	572	17	US-10-449-887A-24	Sequence 24, App
C 44	23.2	80.0	580	9	US-09-815-242-782	Sequence 782, App
C 45	23.2	80.0	580	17	US-10-282-122A-747	Sequence 747, App
C 46	23.2	80.0	617	18	US-10-021-323-5496	Sequence 5496, App
C 47	23.2	80.0	628	17	US-10-282-122A-11485	Sequence 11485, App
C 48	23.2	80.0	656	9	US-09-939-980-87	Sequence 87, App
C 49	23.2	80.0	705	17	US-10-282-122A-16207	Sequence 16207, App
C 50	23.2	80.0	705	17	US-10-424-559-12845	Sequence 12845, App
C 51	23.2	80.0	748	18	US-10-437-963-56273	Sequence 56273, App
C 52	23.2	80.0	840	17	US-10-424-599-105909	Sequence 105909, App
C 53	23.2	80.0	846	17	US-10-282-122A-21226	Sequence 21226, App
C 54	23.2	80.0	884	18	US-10-425-111-1132	Sequence 1132, App
C 55	23.2	80.0	888	10	US-09-989-643-150	Sequence 150, App
C 56	23.2	80.0	888	18	US-10-753-169-150	Sequence 150, App
C 57	23.2	80.0	891	10	US-09-989-643-153	Sequence 153, App
C 58	23.2	80.0	891	10	US-09-989-643-154	Sequence 154, App
C 59	23.2	80.0	891	10	US-09-989-643-157	Sequence 157, App
C 60	23.2	80.0	891	10	US-09-989-643-159	Sequence 159, App
C 61	23.2	80.0	891	10	US-09-989-643-160	Sequence 160, App
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C 63	23.2	80.0	891	10	US-09-989-643-162	Sequence 162, App
C 64	23.2	80.0	891	10	US-09-989-643-163	Sequence 163, App
C 65	23.2	80.0	891	10	US-09-989-643-164	Sequence 164, App
C 66	23.2	80.0	891	10	US-09-989-643-170	Sequence 170, App
C 67	23.2	80.0	891	18	US-10-753-169-153	Sequence 153, App
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C 70	23.2	80.0	891	18	US-10-753-169-159	Sequence 159, App
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C 73	23.2	80.0	891	18	US-10-753-169-162	Sequence 162, App
C 74	23.2	80.0	891	18	US-10-753-169-163	Sequence 163, App
C 75	23.2	80.0	891	18	US-10-753-169-164	Sequence 164, App
C 76	23.2	80.0	891	18	US-10-753-169-166	Sequence 166, App
C 77	23.2	80.0	894	10	US-09-989-643-151	Sequence 151, App
C 78	23.2	80.0	894	10	US-09-989-643-156	Sequence 156, App
C 79	23.2	80.0	894	10	US-09-989-643-167	Sequence 167, App
C 80	23.2	80.0	894	10	US-09-989-643-169	Sequence 169, App
C 81	23.2	80.0	894	18	US-10-753-169-151	Sequence 151, App
C 82	23.2	80.0	894	18	US-10-753-169-156	Sequence 156, App
C 83	23.2	80.0	894	18	US-10-753-169-167	Sequence 167, App
C 84	23.2	80.0	894	18	US-10-753-169-169	Sequence 169, App

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OM nucleic - nucleic search, using sw model

Run on: March 16, 2005, 01:07:34 ; Search time 109.865 Seconds
(without alignments)
431.911 Million cell updates/sec

Title: US-10-089-177-664

Perfect score: 29

Sequence: 1 aayacgatnagngcngcncarcatgca 29

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

1: Issued Patents NA:*

2: /cgn2_6/prodata/1/ina/5A COMB. seq:*

3: /cgn2_6/prodata/1/ina/5B COMB. seq:*

4: /cgn2_6/prodata/1/ina/6A COMB. seq:*

5: /cgn2_6/prodata/1/ina/6B COMB. seq:*

6: /cgn2_6/prodata/1/ina/6C COMB. seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	23.2	80.0	656 3	US-08-936-165A-87 Sequence 87, Appl
2	23.2	80.0	690 4	US-09-543-681A-2724 Sequence 2724, Ap
3	23.2	80.0	864 4	US-09-107-433-1775 Sequence 1775, Ap
4	23.2	80.0	929 4	US-09-710-279-1311 Sequence 1311, Ap
5	23.2	80.0	1113 4	US-09-489-039A-4624 Sequence 4624, Ap
6	23.2	80.0	1122 4	US-09-134-000C-1261 Sequence 1261, Ap
7	23.2	80.0	1131 4	US-09-540-236-22 Sequence 22, Appl
8	23.2	80.0	1131 4	US-09-107-532A-979 Sequence 979, Appl
9	23.2	80.0	1155 2	US-09-328-352-1547 Sequence 1547, Ap
10	23.2	80.0	1185 2	US-08-743-637B-185 Sequence 185, App
11	23.2	80.0	1185 3	US-09-218-197-1 Sequence 1, Appl1
12	23.2	80.0	1185 4	US-09-492-709A-86 Sequence 86, Appl
13	23.2	80.0	1191 4	US-09-107-532A-1379 Sequence 1379, Ap
14	23.2	80.0	1191 4	US-09-902-540-8380 Sequence 8380, Ap
15	23.2	80.0	1197 4	US-09-583-110-747 Sequence 747, Ap
16	23.2	80.0	1224 4	US-09-252-991A-4775 Sequence 4775, Ap
17	23.2	80.0	1230 4	US-09-252-991A-4733 Sequence 4733, Ap
18	23.2	80.0	1230 4	US-09-252-991A-4767 Sequence 2540, Ap
19	23.2	80.0	1245 3	US-09-134-001C-2540 Sequence 2540, Ap
20	23.2	80.0	1254 4	US-09-489-039A-3648 Sequence 3648, Ap
21	23.2	80.0	1260 4	US-09-489-039A-3750 Sequence 3750, Ap
22	23.2	80.0	1356 4	US-09-252-991A-4740 Sequence 4740, Ap
23	23.2	80.0	2277 4	US-09-902-540-3798 Sequence 3798, Ap
24	23.2	80.0	2296 4	US-08-961-527-260 Sequence 260, App
25	23.2	80.0	2297 4	US-09-710-279-3723 Sequence 3723, Ap
26	23.2	80.0	3173 4	US-09-581-822-7 Sequence 7, Appl1
27	23.2	80.0	7035 4	US-09-902-540-878 Sequence 878, App

28	23.2	80.0	15598	4	US-08-956-171E-82	Sequence 82, Appl
29	23.2	80.0	15598	4	US-08-781-986A-82	Sequence 82, Appl
30	23.2	80.0	18551	4	US-09-902-540-1187	Sequence 1187, Appl
31	23.2	80.0	49617	4	US-09-596-002-28	Sequence 28, Appl
32	23.2	80.0	580073	4	US-08-545-528D-1	Sequence 1, Appl1
33	23.2	80.0	640681	4	US-09-790-988-1	Sequence 1, Appl1
34	23.2	80.0	1230025	4	US-09-198-452A-1	Sequence 1, Appl
35	23.2	80.0	1230230	4	US-09-438-185A-1	Sequence 1, Appl
36	23.2	80.0	1830121	4	US-09-557-88A-1	Sequence 1, Appl
37	23.2	80.0	1830121	4	US-09-557-88A-1	Sequence 1, Appl
38	23.2	80.0	1830121	4	US-09-643-990A-1	Sequence 1, Appl
39	23.2	80.0	1830121	4	US-09-643-990A-1	Sequence 1, Appl
40	23.2	80.0	4403765	3	US-09-103-840A-2	Sequence 2, Appl
41	23.2	80.0	4411529	3	US-09-103-840A-2	Sequence 2, Appl
42	21.6	74.5	2552	3	US-09-221-017B-642	Sequence 1, Appl
43	20	69.0	1230	3	US-09-140-466-1	Sequence 1, Appl
44	18.4	63.4	601	4	US-09-949-016-204685	Sequence 204685, Appl
45	18.4	63.4	122626	4	US-09-949-016-17524	Sequence 17524, Appl
46	17.8	61.4	636	4	US-09-543-681A-1862	Sequence 1862, Appl
47	17.4	60.0	601	4	US-09-949-016-136634	Sequence 136634, Appl
48	17.4	60.0	601	4	US-09-949-016-136634	Sequence 1842, Appl
49	17.4	60.0	99629	4	US-09-596-002-37	Sequence 37, Appl
50	17.4	60.0	123463	4	US-09-949-016-17078	Sequence 17078, Appl
51	17.4	60.0	162914	4	US-09-949-016-15578	Sequence 15578, Appl
52	17	58.6	282	4	US-09-313-294A-2082	Sequence 2082, Appl
53	16.8	57.9	1747	4	US-09-949-016-1948	Sequence 1948, Appl
54	16.8	57.9	138282	4	US-09-949-016-15307	Sequence 15307, Appl
55	16.8	57.9	1664976	4	US-08-916-421B-1	Sequence 1, Appl
56	16.8	57.9	1664976	4	US-09-692-570-1	Sequence 1, Appl
57	16.4	56.6	601	4	US-09-949-016-66118	Sequence 66118, Appl
58	16.4	56.6	1266	4	US-09-902-540-2989	Sequence 2989, Appl
59	16.4	56.6	1521	1	US-08-726-136-20	Sequence 20, Appl
60	16.4	56.6	1521	3	US-09-103-434-20	Sequence 20, Appl
61	16.4	56.6	1521	3	US-09-687-594-20	Sequence 20, Appl
62	16.4	56.6	13332	4	US-09-902-540-1047	Sequence 1047, Appl
63	16.4	56.6	13821	4	US-09-949-016-13590	Sequence 13690, Appl
64	16.4	56.6	151089	4	US-09-949-016-14348	Sequence 14348, Appl
65	16.4	56.6	212139	4	US-09-949-016-16065	Sequence 16065, Appl
66	16.4	56.6	524032	4	US-09-949-016-16628	Sequence 16928, Appl
67	16.4	56.6	524032	4	US-09-949-016-16929	Sequence 16929, Appl
68	16.4	56.6	524032	4	US-09-949-016-16930	Sequence 16930, Appl
69	16.4	56.6	524032	4	US-09-949-016-16931	Sequence 16931, Appl
70	16.4	56.6	529885	4	US-09-949-016-14340	Sequence 14340, Appl
71	16.4	56.6	529885	4	US-09-949-016-14341	Sequence 14341, Appl
72	16.4	56.6	529885	4	US-09-949-016-14342	Sequence 14342, Appl
73	16.4	56.6	529885	4	US-09-949-016-14343	Sequence 14343, Appl
74	16.4	56.6	529885	4	US-09-949-016-14344	Sequence 14344, Appl
75	16.4	56.6	529885	4	US-09-949-016-14345	Sequence 14345, Appl
76	16.4	56.6	529885	4	US-09-949-016-14346	Sequence 14346, Appl
77	16.4	56.6	529885	4	US-09-949-016-14347	Sequence 14347, Appl
78	16.4	56.6	4403765	3	US-09-103-840A-2	Sequence 2, Appl
79	16.4	56.6	4411529	3	US-09-103-840A-1	Sequence 1, Appl
80	16.2	55.9	25	4	US-09-396-196G-119074	Sequence 119074, Appl
81	16.2	55.9	1020	4	US-09-328-352-2425	Sequence 2425, Appl
82	16.2	55.9	1125	4	US-09-489-039A-3129	Sequence 3129, Appl
83	16.2	55.9	1248	4	US-09-328-352-2304	Sequence 2304, Appl
84	16.2	55.9	4736	4	US-09-526-192A-15	Sequence 15, Appl
85	16.2	55.9	254366	4	US-09-822-871-3	Sequence 3, Appl
86	16	55.2	984	4	US-09-934-901-1	Sequence 1, Appl
87	16	55.2	984	4	US-09-934-901-1	Sequence 11, Appl
88	16	55.2	984	4	US-10-321-210-1	Sequence 1, Appl
89	16	55.2	984	4	US-10-321-210-1	Sequence 1, Appl
90	16	55.2	174029	4	US-09-949-016-18610	Sequence 12610, Appl
91	16	55.2	174030	4	US-09-949-016-18610	Sequence 12610, Appl
92	15.8	54.5	162	4	US-09-513-999C-29032	Sequence 29032, Appl
93	15.8	54.5	329	3	US-09-060-756-573	Sequence 573, Appl
94	15.8	54.5	329	3	US-09-060-756-573	Sequence 573, Appl
95	15.8	54.5	431	3	US-09-060-756-5539	Sequence 539, Appl
96	15.8	54.5	431	3	US-09-060-756-5539	Sequence 539, Appl
97	15.8	54.5	431	3	US-09-060-756-5539	Sequence 539, Appl
98	15.8	54.5	431	3	US-09-060-756-5539	Sequence 539, Appl
99	15.8	54.5	601	4	US-09-949-016-18205	Sequence 18205, Appl
100	15.8	54.5	601	4	US-09-949-016-18205	Sequence 18205, Appl

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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 22:27:13 ; Search time 2915.62 Seconds
(without alignments)
378.604 Million cell updates/sec

Title: US-10-089-177-664

Perfect score: 29

Sequence: 1 aaygatnagngngcngcncaratgga 29

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gse1: *
9: gb_gse2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	23.2	80.0	114	6	CB261364 02-B5570-
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4	23.2	80.0	160	4	BG895149 358356 MA
5	23.2	80.0	162	4	BI537234 396910 MA
6	23.2	80.0	174	1	AV414173 396910 MA
7	23.2	80.0	175	4	BU162805 396910 MA
8	23.2	80.0	194	8	CC059143 111906.b
9	23.2	80.0	210	2	AM063192 TM0356 KR
10	23.2	80.0	220	9	CL898923 ABG52F11.
11	23.2	80.0	233	7	CF644038 K16_B02_F
12	23.2	80.0	266	1	AV418215 396910 MA
13	23.2	80.0	276	2	AM694494 NF077A05S
14	23.2	80.0	313	7	CN929943 00031AFB
15	23.2	80.0	328	9	CL898925 ABG52F12.
16	23.2	80.0	344	2	AM063346 TM0719 KR
17	23.2	80.0	347	7	CF858624 PBZG001XG
18	23.2	80.0	350	7	T43567 6830_Lambda
19	23.2	80.0	352	7	CV513029 T9ESTzyr8
20	23.2	80.0	354	7	CR476346 CR476346
21	23.2	80.0	355	1	AI486103 EST244424
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38	23.2	80.0	446	1	AV422863
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51	23.2	80.0	471	1	AV422343
52	23.2	80.0	474	8	BZ402639
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56	23.2	80.0	479	4	BI267993
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60	23.2	80.0	482	2	BF639445
61	23.2	80.0	485	1	AU060781
62	23.2	80.0	488	6	CD275520
63	23.2	80.0	490	4	BU803085
64	23.2	80.0	491	1	AU197422
65	23.2	80.0	492	5	BO488762
66	23.2	80.0	493	7	CN547132
67	23.2	80.0	495	2	BE458790
68	23.2	80.0	496	5	BE070882
69	23.2	80.0	497	6	CB279706
70	23.2	80.0	497	6	CD658495
71	23.2	80.0	498	7	CF606638
72	23.2	80.0	501	7	CO746459
73	23.2	80.0	502	4	BU803992
74	23.2	80.0	505	7	CK994878
75	23.2	80.0	510	6	CB331112
76	23.2	80.0	510	2	BE921734
77	23.2	80.0	511	4	BG465515
78	23.2	80.0	511	2	AM675933
79	23.2	80.0	512	4	BM323718
80	23.2	80.0	514	4	BU758011
81	23.2	80.0	515	1	AV940645
82	23.2	80.0	516	6	CA524936
83	23.2	80.0	516	6	CD272559
84	23.2	80.0	516	9	AG267461
85	23.2	80.0	517	5	BO791087
86	23.2	80.0	518	1	AL813000
87	23.2	80.0	518	1	AV442731
88	23.2	80.0	518	2	AM257991
89	23.2	80.0	518	2	BE494337
90	23.2	80.0	518	2	TA233908P
91	23.2	80.0	519	5	BP039049
92	23.2	80.0	519	6	CA905535
93	23.2	80.0	522	1	AV917158
94	23.2	80.0	524	4	BM066124
95	23.2	80.0	525	4	BG904292
96	23.2	80.0	526	8	AZ302919
97	23.2	80.0	527	6	CB331196

AV551304	AV551304
CB655390	OSJNRC08M
T04276	3.23_Lambda-m
AV518885	AV518885
BE521145	MT1734STM
AU289247	AU289247
BG263014	WHE0939_0306
BH749989	SALK_0306
BO622855	CC_Config
BM402658	SLA007C01
AV408359	AV408359
AM040690	EST283554
BU993125	HD12K10r
AV422863	AV422863
BE354313	EST355656
AZ326080	476_dio40
AM907286	EST343409
CA516269	KS09055F1
M89271	CEL20D1 Chr
BZ349218	hg88604.g
AI483744	EST249615
CL903283	ACAB272/A
AV940013	AV940013
CD275318	T143B0287
CO052070	MdFw20561
CL903282	ACAB272/A
AV422343	AV422343
BZ402639	OGAA236TM
CN942360	010920AVB
BZ402631	OGAA236TC
BI704013	kt65d06.y
BI267993	NE11D041
CV042450	ta156b07.
AZ049142	GSSBR1054
AI778328	EST259207
BF639445	NF013F081
AU060781	AU060781
CD275520	T143B0155
BU803085	BU803085
AU197422	AU197422
BO488762	19-B8455-
CN547132	EST_15121
BE458790	EST414082
BE070882	BE070882
CB279706	tu85g06.y
CD658495	EESTeE34
CF606638	GEMMA01.0
CO746459	cah90f12.
BU803992	BU803992
CK994878	041C04R1.
CB331112	3529_1_33
BE921734	EST425503
BG465515	RH122_45
AM675933	EST6_10937
BM323718	PIC1_22_E
BU758011	BU758011
AV940645	AV940645
CA524936	KS12045E1
CD272559	T143B0653
AG267461	Cyantiid108
BO791087	E3907_Chl
AL813000	AL813000
AV442731	AV442731
AM257991	687065D08
BE494337	WHE1253_D
TA233908P	TA233908P
BP039049	BP039049
CA905535	PCSC16701
AV917158	AV917158
BM066124	KS07011A0
BG904292	Talr1131A
AZ302919	GSSBR186
CB331196	3529_1_34

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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 15:46:58 ; Search time 373.654 Seconds
(without alignments)
459.443 Million cell updates/sec

Title: US-10-089-177-664

Perfect score: 29

Sequence: 1 aayatgatnaacngngcngncarctgga 29

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : N_Geneseq_1dec04:*

1: Geneseq1980s:*\n2: Geneseq1990s:*\n3: Geneseq2000s:*\n4: Geneseq2001as:*\n5: Geneseq2001bs:*\n6: Geneseq2002as:*\n7: Geneseq2002bs:*\n8: Geneseq2003as:*\n9: Geneseq2003bs:*\n10: Geneseq2003cs:*\n11: Geneseq2003ds:*\n12: Geneseq2004as:*\n13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	23.2	80.0	29	AAV37106	Aav37106 Oligonuc
2	23.2	80.0	29	AAH00673	Aah00673 Universal
3	23.2	80.0	29	ACR05433	Act05433 Universal
4	23.2	80.0	70	ACA14649	Act14649 Prokaryot
5	23.2	80.0	70	ACA14091	Act14091 Prokaryot
6	23.2	80.0	70	ACA14857	Act14857 Prokaryot
7	23.2	80.0	111	ACA14506	Act14506 Prokaryot
8	23.2	80.0	130	AAS50396	Aas50396 Staphyloc
9	23.2	80.0	130	ACA17665	Act17665 Prokaryot
10	23.2	80.0	163	AAS47684	Aas47684 Enterococ
11	23.2	80.0	163	ACA12386	Act12386 Prokaryot
12	23.2	80.0	183	ACA14546	Act14546 Staphyloc
13	23.2	80.0	184	AAS49608	Aas49608 Staphyloc
14	23.2	80.0	184	ACA16888	Act16888 Prokaryot
15	23.2	80.0	185	ACA14269	Act14269 Prokaryot
16	23.2	80.0	185	ACA13966	Act13966 Prokaryot
17	23.2	80.0	187	AAS47621	Aas47621 Enterococ
18	23.2	80.0	187	AAS47617	Aas47617 Enterococ
19	23.2	80.0	187	ACA12332	Act12332 Prokaryot
20	23.2	80.0	187	ACA12314	Act12314 Prokaryot

21	23.2	80.0	193	ACA14683	Act14683 Prokaryot
22	23.2	80.0	196	ACA15526	Act15526 Prokaryot
23	23.2	80.0	202	AAS47599	Aas47599 Enterococ
24	23.2	80.0	202	ACA12394	Act12394 Prokaryot
25	23.2	80.0	222	ACA13907	Act13907 Prokaryot
26	23.2	80.0	222	ACA14700	Act14700 Prokaryot
27	23.2	80.0	236	AAS47724	Aas47724 Enterococ
28	23.2	80.0	236	ACA12410	Act12410 Prokaryot
29	23.2	80.0	269	AAS47665	Aas47665 Enterococ
30	23.2	80.0	269	ACA12359	Act12359 Prokaryot
31	23.2	80.0	275	ACA14082	Act14082 Prokaryot
32	23.2	80.0	275	ACA14835	Act14835 Prokaryot
33	23.2	80.0	275	ACA13919	Act13919 Prokaryot
34	23.2	80.0	277	ABL71031	Ab171031 Corn taas
35	23.2	80.0	329	ACA14838	Act14838 Prokaryot
36	23.2	80.0	332	ACA14276	Act14276 Prokaryot
37	23.2	80.0	341	ACA14524	Act14524 Prokaryot
38	23.2	80.0	341	ACA14657	Act14657 Prokaryot
39	23.2	80.0	343	ACA14063	Act14063 Prokaryot
40	23.2	80.0	385	AAH89749	Aah89749 Synthetic
41	23.2	80.0	390	ACA14749	Act14749 Prokaryot
42	23.2	80.0	467	ACA15425	Act15425 DNA clone
43	23.2	80.0	515	ACA15426	Act15426 DNA clone
44	23.2	80.0	532	ACA15433	Act15433 DNA clone
45	23.2	80.0	566	ACA13141	Act13141 Prokaryot
46	23.2	80.0	572	ADD28534	Add28534 Mouse cae
47	23.2	80.0	580	AAS48205	Aas48205 Enterococ
48	23.2	80.0	580	ACA12877	Act12877 Prokaryot
49	23.2	80.0	606	ACA15431	Act15431 DNA clone
50	23.2	80.0	608	ACA15428	Act15428 DNA clone
51	23.2	80.0	617	ACN50715	Acn50715 Cotton an
52	23.2	80.0	628	ACA23615	Act23615 Prokaryot
53	23.2	80.0	652	ABX66890	Abx66890 Helicobac
54	23.2	80.0	656	AAT83947	Aat83947 DNA encod
55	23.2	80.0	656	AAV53387	Aav53387 DNA encod
56	23.2	80.0	657	ABZ41637	Abz41637 N. gonorr
57	23.2	80.0	657	10 ABZ41137	Abz41137 N. gonorr
58	23.2	80.0	662	ABX66333	Abx66333 Helicobac
59	23.2	80.0	690	ADF02439	Adf02439 Bacteriat
60	23.2	80.0	705	ACA28337	Act28337 Prokaryot
61	23.2	80.0	720	ABZ41639	Abz41639 N. gonorr
62	23.2	80.0	744	ABZ41141	Abz41141 N. gonorr
63	23.2	80.0	744	5 AAS81943	Aas81943 DNA encod
64	23.2	80.0	779	10 ACFe6884	Acfe6884 Phototrab
65	23.2	80.0	846	ACA33356	Act33356 Prokaryot
66	23.2	80.0	864	ADR93140	Adr93140 Novel S.
67	23.2	80.0	888	AAV37149	Aav37149 DNA sequ
68	23.2	80.0	888	AAH01744	Aah01744 Borrellia
69	23.2	80.0	891	AAV37160	Aav37160 DNA sequ
70	23.2	80.0	891	AAV37152	Aav37152 DNA sequ
71	23.2	80.0	891	AAV37156	Aav37156 DNA sequ
72	23.2	80.0	891	AAV37163	Aav37163 DNA sequ
73	23.2	80.0	891	AAV37169	Aav37169 DNA sequ
74	23.2	80.0	891	AAV37153	Aav37153 DNA sequ
75	23.2	80.0	891	AAV37161	Aav37161 DNA sequ
76	23.2	80.0	891	AAV37158	Aav37158 DNA sequ
77	23.2	80.0	891	AAV37159	Aav37159 DNA sequ
78	23.2	80.0	891	AAV37162	Aav37162 DNA sequ
79	23.2	80.0	891	AAH01750	Aah01750 Micrococ
80	23.2	80.0	891	AAH01754	Aah01754 Rickettsi
81	23.2	80.0	891	AAH01752	Aah01752 Mycoplasma
82	23.2	80.0	891	AAH01675	Aah01675 Escherich
83	23.2	80.0	891	AAH01753	Aah01753 Neisseria
84	23.2	80.0	891	AAH01751	Aah01751 Mycobacte
85	23.2	80.0	891	AAH00619	Aah00619 Haemophil
86	23.2	80.0	891	AAH01755	Aah01755 Salmonell
87	23.2	80.0	891	AAH01760	Aah01760 Ureaplasma
88	23.2	80.0	894	AAV37155	Aav37155 DNA sequ
89	23.2	80.0	894	AAV37150	Aav37150 DNA sequ
90	23.2	80.0	894	AAV37168	Aav37168 DNA sequ
91	23.2	80.0	894	AAV37166	Aav37166 DNA sequ
92	23.2	80.0	894	2 AAV37166	Aav37166 DNA sequ
93	23.2	80.0	894	4 AAH01759	Aah01759 Treponema

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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 22:08:52 ; Search time 1102.56 Seconds
(without alignments)
1274.492 Million cell updates/sec

Title: US-10-089-177-664

Perfect score: 29

Sequence: 1 aayatgatnagngngngncaratagga 29

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_bhg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_to:*
11: gb_ets:*
12: gb_ey:*
13: gb_un:*
14: gb_vt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23.2	80.0	29	6	AX109931 Sequence
2	23.2	80.0	29	6	BD023039 Sequence
3	23.2	80.0	385	6	BD137176 Autonomou
4	23.2	80.0	652	6	AX790513 Sequence
5	23.2	80.0	654	1	AB025429 Synchoco
6	23.2	80.0	654	1	AB025430 Synchoco
7	23.2	80.0	656	6	AR194538 Sequence
8	23.2	80.0	662	6	AX789399 Sequence
9	23.2	80.0	688	1	GVU09433 Sequence
10	23.2	80.0	690	6	AR377718 Sequence
11	23.2	80.0	700	1	AY661424 Candidatu
12	23.2	80.0	700	1	AY685053 Candidatu
13	23.2	80.0	703	1	PHU09445 Prochloroth
14	23.2	80.0	703	8	BFU09442 Pandorina m
15	23.2	80.0	705	8	BFU09424 Bryopsis pl
16	23.2	80.0	705	8	CCU09429 Costaria co
17	23.2	80.0	705	8	CSU09426 Chlorella s
18	23.2	80.0	705	8	DMU09431 Derbesia ma
19	23.2	80.0	705	8	SMU09447 Smitthora na

20	23.2	80.0	706	1	GSU09434 Gloeotheca
21	23.2	80.0	706	1	PEU09443 Phormidium
22	23.2	80.0	706	8	DEU09432 Diaparnaldi
23	23.2	80.0	706	8	GLU09436 Gracilaria
24	23.2	80.0	706	8	GPU09435 Gonium pect
25	23.2	80.0	706	8	LSU09437 Laminaria s
26	23.2	80.0	706	8	MSU09438 Mantoniella
27	23.2	80.0	706	8	ODU09440 Ochomonas
28	23.2	80.0	706	8	OSU09441 Odontella s
29	23.2	80.0	706	8	PSU09449 Porphyridiu
30	23.2	80.0	706	8	VSU09448 Vaucheria b
31	23.2	80.0	709	1	NSU09439 Nitzelia tra
32	23.2	80.0	732	1	AF217548 Buchnera
33	23.2	80.0	732	1	AF217549 Buchnera
34	23.2	80.0	732	1	AF217550 Buchnera
35	23.2	80.0	732	1	AF217551 Buchnera
36	23.2	80.0	732	1	AF217552 Buchnera
37	23.2	80.0	747	8	CBS544127 Calcidisc
38	23.2	80.0	747	8	CBS544125 Calcidisc
39	23.2	80.0	747	8	CBS544126 Calcidisc
40	23.2	80.0	747	8	CBS544128 Calcidisc
41	23.2	80.0	747	8	CBS544124 Calcidisc
42	23.2	80.0	747	8	HCAS44134 Helicosp
43	23.2	80.0	747	8	HYAS44133 Helicosp
44	23.2	80.0	747	8	PCAS44131 Pleurochr
45	23.2	80.0	747	8	PDS44132 Pleurochr
46	23.2	80.0	747	8	UF0544130 Umbilicos
47	23.2	80.0	747	8	US1544129 Umbilicos
48	23.2	80.0	768	1	AY303553 Candidatu
49	23.2	80.0	798	1	AY303555 Candidatu
50	23.2	80.0	802	1	AB095495 Aster yel
51	23.2	80.0	802	1	AB095667 Aster yel
52	23.2	80.0	802	1	AB095668 Aster yel
53	23.2	80.0	802	1	AB095669 Aster yel
54	23.2	80.0	802	1	AB095670 Aster yel
55	23.2	80.0	802	1	AB095671 Aster yel
56	23.2	80.0	802	1	AB095672 Aster yel
57	23.2	80.0	802	1	AB095673 Tsuwabuki
58	23.2	80.0	804	1	AB095674 Western X
59	23.2	80.0	804	1	AY303556 Candidatu
60	23.2	80.0	804	1	AY303571 Candidatu
61	23.2	80.0	805	1	PSY18215 Papaya dieb
62	23.2	80.0	812	1	AR465542 Buchnera
63	23.2	80.0	858	8	AT391373 Galdieria
64	23.2	80.0	862	1	AY303552 Candidatu
65	23.2	80.0	862	1	AY303554 Candidatu
66	23.2	80.0	867	1	AY454403 Percussar
67	23.2	80.0	870	8	AY566054 Pinnus kor
68	23.2	80.0	875	8	AY454409 Acrochaet
69	23.2	80.0	879	8	AY454417 Halochlor
70	23.2	80.0	880	8	AY454418 Bolbocole
71	23.2	80.0	881	8	AY454412 Acrochaet
72	23.2	80.0	882	8	AY454415 Phaeophili
73	23.2	80.0	882	8	AY568053 Klebsorni
74	23.2	80.0	883	8	AY454419 Bolbocole
75	23.2	80.0	884	8	AY454422 Psuedonoe
76	23.2	80.0	885	8	AY454416 Phaeophili
77	23.2	80.0	886	6	AY454424 Ulothrrix
78	23.2	80.0	888	6	AX111004 Sequence
79	23.2	80.0	888	6	BD023082 Species-s
80	23.2	80.0	891	6	AX109877 Sequence
81	23.2	80.0	891	6	AX110935 Sequence
82	23.2	80.0	891	6	AX111010 Sequence
83	23.2	80.0	891	6	AX111011 Sequence
84	23.2	80.0	891	6	AX111012 Sequence
85	23.2	80.0	891	6	AX111013 Sequence
86	23.2	80.0	891	6	AX111014 Sequence
87	23.2	80.0	891	6	AX111015 Sequence
88	23.2	80.0	891	6	AX111020 Sequence
89	23.2	80.0	891	6	BD023085 Species-s
90	23.2	80.0	891	6	BD023086 Species-s
91	23.2	80.0	891	6	BD023089 Species-s
92	23.2	80.0	891	6	BD023091 Species-s